LANDSCAPE GENETICS OF FERAL SWINE AND IMPLICATIONS FOR MANAGEMENT

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Abstract: The management of the invasive feral pig (*Sus scrofa*) has been the subject of intense study in recent years. Feral pigs are also susceptible to diseases (e.g., brucellosis, pseudorabies) that can be transmitted to livestock, humans, and wildlife. Feral pigs clearly represent a threat to the sustainability of multiple agriculture products. Population reduction (trapping or shooting) is the best current alternative for controlling pig damage. However, reduction is crude and inefficient in terms of manpower and resources because pigs from neighboring areas quickly recolonize managed areas. We used a panel of 9 microsatellite loci to study broad-scale population structure in feral pigs from south Texas and to evaluate recolonization after a local removal. At a broad scale (>200 km), pig populations displayed a moderate degree of genetic structure (Fst = 0.16), suggesting that at broad geographic scales, populations are differentiated enough to be functionally independent. However, genetic similarity was not a simple function of geographic distance, implying that movement and dispersal are not equal among populations. This may be due to the presence of terrain features that promote (e.g., river systems) or inhibit (e.g., urban areas, farmland areas) dispersal. At a local scale, animal samples taken before and after a removal event were genetically different (Fst = 0.08), indicating rapid recolonization occurred into the controlled area. Overall, our results indicate that knowledge of population structure in south Texas could be used to improve pig control efforts, but high rates of movement and dispersal in other areas would likely require control efforts over a very broad region, possibly an entire watershed. Ongoing efforts will attempt to identify fine-scale genetic structure and landscape features that could be used to focus management efforts.

Key Words: damage management, feral pig, genetics, invasive species, population management, *Sus scrofa*.

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Feral pigs (*Sus scrofa*) are considered an exotic invasive in the United States, where conservative estimates indicate an annual loss of $200/pig due to agricultural damage. Feral pigs may have dramatic effects on native ecosystems by excessive rooting and wallowing (Taylor 1993). Feral pigs compete with and predate upon wildlife and livestock species (Synatzske 1979, Taylor 1993, Tolleson et al. 1993, Gipson et al. 1998, Kammermeyer et al. 2003). Finally, feral pigs are also susceptible to diseases that can be transmitted to livestock, humans, and wildlife, including pseudorabies, swine brucellosis, bovine tuberculosis, vesicular stomatitis, and leptospirosis, as well as foreign animal diseases, such as foot and mouth disease, rinderpest, African swine fever, or classical swine fever (Witmer et al. 2003).

Feral pigs clearly represent a threat to the sustainability of multiple agriculture products and natural resources. Population reduction (trapping or shooting) is the best current alternative for controlling pig damage. However, reduction is inefficient in terms of manpower and resources because pigs from neighboring areas quickly re-colonize managed areas. In addition, trapping and shooting methods have a reduced success over time and limited area of population impact (Mapston 2004). Increased knowledge of pig movements and population structuring could dramatically improve the efficiency of management efforts by focusing manpower and resources where they are most effective. For instance, landscape features that influence pig movements could be incorporated into control efforts. Targeting dispersal corridors could prevent re-colonization of managed areas or natural boundaries could be used in a “divide and conquer” strategy. In other cases, the landscape could be altered to prevent immigration.

Furthermore, the scale of management could be adjusted to match the entire population of interest, perhaps by encouraging the formation of management cooperatives in areas where the scale of the population exceeds the average size of landholdings.

Traditional wildlife approaches, including telemetry, tagging, etc., are informative, but costly and limited by sample size and study duration (DeYoung and Honeycutt 2005). Population genetic approaches consider the numerous demographic and stochastic factors affecting population structure and connectivity in a well-developed theoretical framework. However, the application of population genetic theory to wildlife management problems was long limited by a lack of suitable genetic markers and the time and cost-intensive nature of the laboratory methods (DeYoung 2007). A suite of technological advances during the past two decades have resulted in dramatic gains in the number and types of molecular markers, automation of laboratory instrumentation, and increased computer processing speed. Therefore, large-scale genetic studies of wildlife populations are now feasible and offer a powerful new tool for wildlife management (DeYoung and Honeycutt 2005, DeYoung 2007). For instance, the combination of genetic data with geographic information systems (GIS) provides the capability to directly assess the influence of landscape features on population structure and rates of gene flow (Manel et al. 2003).

We are using a panel of microsatellite DNA loci in a landscape-genetic approach to study broad-scale population structure in feral pig populations in south Texas. Our preliminary data indicates that at a broad geographical scale, pig populations display a moderate degree of genetic structure, suggesting that disjunct populations are differentiated enough to be functionally independent. However, genetic and geographic distances among populations do not follow a simple linear relationship. Some geographically proximate populations are genetically dissimilar, while some geographically distant populations are similar. Consequently, movement and dispersal are not equal among populations. Patterns of genetic similarity or dissimilarity among populations are correlated to the presence of terrain features that promote (e.g., river systems) or inhibit (e.g., urban areas, farmland areas) dispersal. Overall, our preliminary results indicate that knowledge of population structure in south Texas could be used to improve pig control efforts. Ongoing efforts will attempt to identify fine-scale genetic structure and landscape features that could be used to focus management efforts.

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LITERATURE CITED

DEYOUNG, R. W. 2007. Genetics and applied management: using genetic methods to solve emerging wildlife management problems. Pages 317-336 *in* T. E. Fulbright and D. G. Hewitt, editors. Frontiers in wildlife science: linking ecological theory and management applications. CRC Press, Boca Raton, Florida, USA.

DEYOUNG, R. W., AND R. L. HONEYCUTT. 2005. The molecular toolbox: genetic techniques in wildlife ecology and management. Journal of Wildlife Management 69:1362-1384.

GIPSON, P. S., B. HLAVACHICK, AND T. BERGER. 1998. Range expansion by wild hogs across the central United States. Wildlife Society Bulletin 26:279-286.

KAMMERMEYER, K., J. BOWERS, B. COOPER, D. FORSTER, K GRAHL, T. HOLBROOK, C. MARTIN, S. MCDONALD, N. NICHOLSON, M. VANBRACKLE, AND G. WATERS. 2003. Feral hogs in Georgia: disease, damage and control. Georgia Department of Natural Resources, Wildlife Resources Division, Game Management Section, Social Circle, Georgia, USA.

MANEL, S., M. K. SCHWARTZ, G. LUIKART, AND P. TABERLET. 2003. Landscape genetics: combining landscape ecology and population genetics. Trends in Ecology and Evolution 18:189-197.

MAPSTON, M. E. 2004. Feral hogs in Texas. Texas Cooperative Extension, Texas A&M University Press, College Station, Texas, USA.

SYNATZSKE, D. R. 1979. Status of the feral hog in Texas. Texas Parks and Wildlife Department, Artesia Wells, Texas, USA.

TAYLOR, R. B. 1993. History and distribution of feral hogs in Texas. Pages 17-27 *in* C. W. Hanselka and J. F. Cadenhead, editors. Feral swine: a compendium for resource managers: proceedings of a conference. Texas Agricultural Extension Service, College Station, Texas, USA.

TOLLESON, D., D. ROLLINS, W. PINCHAK, M. IVY, AND A. HIERMAN. 1993. Impact of feral hogs on ground-nesting gamebirds. Pages 76-83 *in* C. W. Hanselka and J. F. Cadenhead, editors. Feral swine: a compendium for resource managers: proceedings of a conference. Texas Agricultural Extension Service, College Station, Texas, USA.

WITMER, G. W., R. B. SANDERS, AND A. C. TAFT. 2003. Feral swine-are they a disease threat to livestock in the United States? Proceedings of the Wildlife Damage Management Conference 10:316-325.